



Blast 2 Sequences results

Public

Enter

BLAST

OMIM

Taxonomy

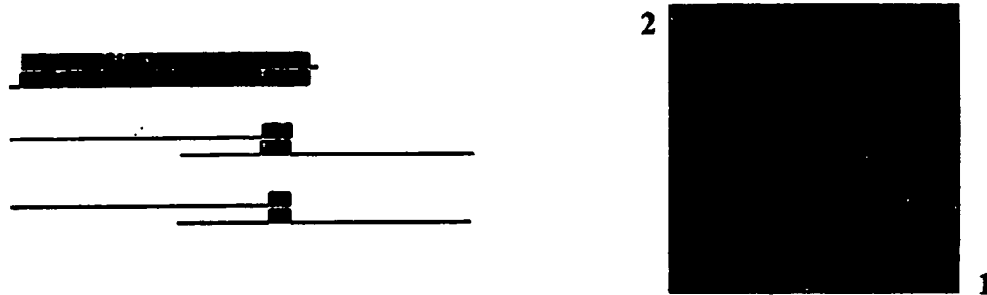
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 gi **18579009** tumor rejection antigen (gp96) 1 [Homo sapiens] Length 719 (1 .. 719)

Sequence 2 gi **32488** Length 732 (1 .. 732)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 622 bits (1605), Expect = e-177

Identities = 336/715 (46%), Positives = 468/715 (64%), Gaps = 27/715 (3%)

Query: 1 MMKLIINSLYKNKEIFLRELISNASDALDKIRLISLTDENALSGNEELTVKIKCDKEKNL 60
 +M LIIN+ Y NKEIFLRELISN+SDALDKIR +LTD + L +EL + + +K+
 Sbjct: 29 LMSLIINTFYSNKEIFLRELISNSSDALDKIRYETLTDP SKLDSGKELHINLIPNKQDRT 88

Query: 61 LHVTDGTGVMTRBELVKNLGTIAKSGTSEFLNKMTEAQEDGQSTSELIGQFGVGFYSAFL 120
 L + DTG+GMT+ +L+ NLGTIAKSGT F+ EA + G S +IGQFGVGFYSA+L
 Sbjct: 89 LTIVDTGIGMTKADLINNLGTIAKSGTKAFM---EALQAGADIS-MIGQFGVGFYSAYL 143

Query: 121 VADKVIIVTSKHNDTQHIWESDSNEFSVIADPRGNTLGRGTTITLVLKEEASDYLELDTI 180
 VA+KV V +KHND Q+ WES + G +GRGT + L LKE+ ++YLE I
 Sbjct: 144 VAEKVTVITKHNDDEQYAWESSAGGSFTVRTDTGEPMGRGTVILHLKEDQTEYLEERRI 203

Query: 181 KNLVKKYSQFPIFYVWSSKT-----ETVEEPMEEEEAAKEEKEESD----DEAAV 228
 K +VKK+SQFI +PI ++ K E E+ +EEE KEEKE D ++
 Sbjct: 204 KEIVKKHSQFIGYPITL FVEKERDKEVSDDEAEKEKEDKEEKEKEEKESEDKPEIEDVGS 263

Query: 229 EEEEEK---KPKTKKVEKTVWDWELMNDIKPIWQRPSKEVEEDEYKAFYKSFSKESDDP 285
 +EEEE+K K K KK+++ D E +N KPIW R ++ +EY FYKS + + +D
 Sbjct: 264 DEEEKKDGDGDKKKKKIKIKYIDQEELNKTPIWTRNPDDITNBEYGEFYKSLTNDWEDH 323

Query: 286 MAYIHFTAEGEVTFSILFVPTSAPRGLFDEYSGSKSDYIKLYVRRVFIITDDFHDMMPKY 345
 +A HF+ EG++ F+++LFVP AP LF+ KK + IKLYVRRVFI D+ +++P+Y
 Sbjct: 324 LAVKHFSVEGQLEFRALLFVPRRAPFDLFEN--RKKKNNIKLYVRRVFI

Query: 346 LNFVKGVDSDDDLPLNVSRETQQHKLKLVIRKLVKRLTDMIKKIADD
 LNF++GVVDS+DLPLN+SRE LQQ K+LKVIRK LV+K L++ ++A+D
 Sbjct: 382 LNFIRGVVDSDDLPLNISREMLQQSKILKLVIRKLVKRCLELFTELAED

Fordham Exhibit 1041
 University of NM v. Fordham
 Interference No. 104,761



Blast 2 Sequences results

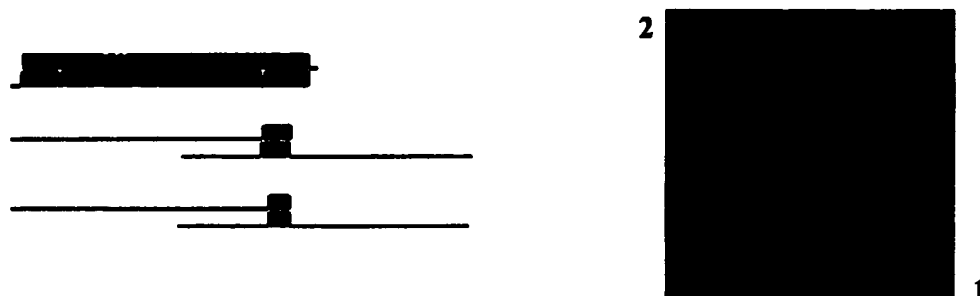
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 gi 18579009 tumor rejection antigen (gp96) 1 [Homo sapiens] Length 719 (1 .. 719)

Sequence 2 gi 32488

Length 732 (1 .. 732)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 622 bits (1605), Expect = e-177

Identities = 336/715 (46%), Positives = 468/715 (64%), Gaps = 27/715 (3%)

```

Query: 1  MMKLIINSLYKNKEIFLRELISNASDALDKIRLISLTDENALSGNEELTVKIKCDKEKNL 60
          +M LIIN+ Y NKEIFLRELISN+SDALDKIR +LTD + L +EL + + +K+
Sbjct: 29  LMSLIINTFYSNKEIFLRELISNSSDALDKIRYETLTDP SKLDSGKELHINLIPNKQDRT 88

Query: 61  LHVTDGTGVMTRBELLVKNLGTIAKSGTSEFLNKMTEAQEDGQSTSELIGQFGVGFYSAFL 120
          L + DTG+GMT+ +L+ NLGTIAKSGT F+ EA + G S +IGQFGVGFYSA+L
Sbjct: 89  LTIVDTGIGMTKADLINNLGTIAKSGTKAFM----EALQAGADIS-MIGQFGVGFYSAYL 143

Query: 121  VADKVIVTSKHNNDTQHIWESDSNEFSVIADPRGNTLGRGTTITLVLKEEASDYLELDTI 180
          VA+KV V +KHN+D Q+ WES + + G +GRGT + L LKE+ ++YLE I
Sbjct: 144  VAEKVTVITKHNDDEQYAWESSAGGSFTVRTDTGEP MGRGTKVILHLKEDQTEYLEERRI 203

Query: 181  KNLVKKYSQFINFPIYVWSSKT-----ETVEEPMEEEEAAKEEKEESD----DEAAV 228
          K +VKK+SQFI +PI ++ K E E+ +BEE KEEKE D ++
Sbjct: 204  KEIVKKHSQFIGYPITLFVEKERDKEVSDDEAEKEKEDKEEKEKEEKESEDKPEIEDVGS 263

Query: 229  EEEEEEEK---KPKTKKVEKTVDWELMNDIKPIWQRPSKEVEEDEYKAFYKSFSKESDDP 285
          +EEEE+K K K KK+++ D E +N KPIW R ++ +EY FYKS + + +D
Sbjct: 264  DEEEEEKDGDKKKKKKIKEYIDQEELNKT KPIWTRNPDDITNEEYGEFYKSLTNDWEDH 323

Query: 286  MAYIHFTAEGEVTFKSI L FVPTSAPRGLFDEYGSKKSDYIKLYVRRVFI TDDFHDMMPKY 345
          +A HF+ EG++ F+++LFVP AP LF+ KK + IKLYVRRVFI D+ +++P+Y
Sbjct: 324  LAVKHFSVEGQLEFRALLFVPRRAPFDLFEN--RKKKNNIKLYVRRVFI MDNCEBELIPEY 381

Query: 346  LNFVKGVDSDDLPLNVSRET LQQHKLLKVIKLVKRLTDMIKKIADDKYN-DTFWKEF 404
          LNF++GVDSD+DLPLN+SRE LQQ K+LKVIRK LV+K L++ ++A+DK N F+++F
Sbjct: 382  LNFIRGVVDSDDLPLNISREMLQQSKILKVIRKNLVKKCLELFTELAEDKENYKKFYEQF 441
  
```

Query: 405 GTNIKLGVIEDHSNRTRLAKLLRFQSSHPTDITSLDQYVERMKKQDKIYFMAGSSRKE 464
 NIKLG+ ED NR +L++LLR+ +S ++ SL Y RMKE Q IY++ G ++ +
 Sbjct: 442 SKNIKLGIIHEDSQNRKKLSELLRYTSASGDEMVSLLKDYCTRMKENQKHIIYYITGETKDQ 501

Query: 465 AESSPFVERLLKKGYEVIYLTPEVDEYCIQALPEFDGKRFQNVAKGKVFDESEKTKESR 524
 +S FVERL K G EVIY+ EP+DEYC+Q L EF+GK +V KEG++ E E+ K+ +
 Sbjct: 502 VANSAPFVERLRKHGLEVIYMIPIDEYCVQQLKEFEGKTLVSVTKEGLELPEDEEEKKKQ 561

Query: 525 EAVEKEFEPLLNWMKDKALKDKIEKAVVSQRLTESPCALVASQYGWSGNMERIMKAQAYQ 584
 E + +FE L MKD L+ K+EK VVS RL SPC +V S YGW+ NMERIMKAQA
 Sbjct: 562 EEKTKTFENLCKIMKD -ILEKKVEKVVVSNRLVTSPCCIVTSTYGWTANMERIMKAQAL- 619

Query: 585 TGKDISTNYIASQKKTFEINPRHPLIRDMRLRIKEDDEDDKTVLDLAVVLFETATLRSGYL 644
 +D ST Y + KK EINH H +I + ++ + D++DK+V DL ++L+ETA L SG+
 Sbjct: 620 --RDNSTMGYMAAKKHLBINPDHSIIETLRQKAEADKNDKSVKDLVILLYETALLSSGFS 677

Query: 645 LPDTKAYGDRIERMLRLSLNIDPDAKVEEPEEPEEPTAEDTTEDTEQDEDEEMD 699
 L D + + +RI RM++L L ID D ++ E D + EE+D
 Sbjct: 678 LEDPQTHANRIYRMIKLGLGIDEDDPTADDTSAAVTEEMPPLEGDDDTSRMEFVD 732

Score = 35.4 bits (80), Expect = 3.4
 Identities = 21/73 (28%), Positives = 38/73 (51%), Gaps = 2/73 (2%)

Query: 649 KAYGDRIERMLRLSLNIDPDAKVEEPEEPEEPTAEDTTEDTEQDEDE--EEMDVGTDDEE 706
 K + I + L + + D +V ++ EE E+ E+ ++ ++ ED E DVG+DEEE
 Sbjct: 208 KKHSQFIGYPITLFEKERDKEVSDDEAEKEDKEEKEKEEKESEDKPEIEDVGSDEEE 267

Query: 707 ETAKESTAEDKDEL 719
 E +K ++
 Sbjct: 268 EKKDGDKKKKKKI 280

Score = 34.7 bits (78), Expect = 5.9
 Identities = 17/54 (31%), Positives = 30/54 (55%)

Query: 666 DPAKVEEPEEPEEPTAEDTTEDTEQDEDEEMDVGTDDEEEETAKESTAEDKDEL 719
 + + K EE+ +EE E + ED DE+EE G ++++ KE +++EL
 Sbjct: 237 EKEDKEEKEKEEKESEDKPEIEDVGSDEEEKKDGDKKKKKKIKEYIDQSEL 290

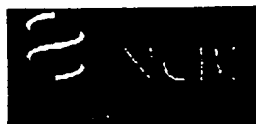
CPU time: 0.19 user secs. 0.02 sys. secs 0.21 total secs.

Lambda K H
 0.311 0.131 0.359

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 10,211
 Number of Sequences: 0
 Number of extensions: 755
 Number of successful extensions: 62
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 5
length of query: 719
length of database: 330,426,180
effective HSP length: 131
effective length of query: 588
effective length of database: 270,223,427
effective search space: 158891375076
effective search space used: 158891375076
T: 9
A: 40
X1: 16 (7.2 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (21.8 bits)
S2: 77 (34.3 bits)

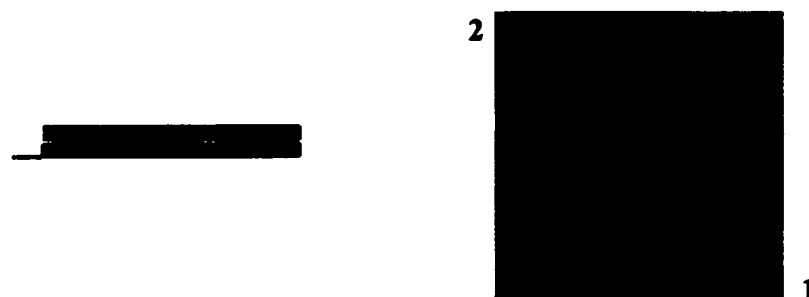


Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 gi_18579009 tumor rejection antigen (gp96) 1 [Homo sapiens] Length 719 (1..719)
Sequence 2 gi_119360 Endoplasmic precursor (94 kDa glucose-regulated protein) (GRP94) (gp96 homolog) (Tumor rejection antigen 1). Length 803 (1..803)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1425 bits (3690), Expect = 0.0
Identities = 719/719 (100%), Positives = 719/719 (100%)

```
Query:      1  MMKLIINSLYKNKEIFLRELISNASDALDKIRLISLTDENALSGNEELTVKIKCDKEKNL  60
             MMKLIINSLYKNKEIFLRELISNASDALDKIRLISLTDENALSGNEELTVKIKCDKEKNL
Sbjct:     85  MMKLIINSLYKNKEIFLRELISNASDALDKIRLISLTDENALSGNEELTVKIKCDKEKNL 144
glycosylation 107
TRAI       85  ++++++
Mature chain 85  *****

Query:     61  LHVTDTGVGMTREELVKNLGTIAKSGTSEFLNKMTEAQEDGQSTSELIGQFGVGFYSAFL 120
             LHVTDTGVGMTREELVKNLGTIAKSGTSEFLNKMTEAQEDGQSTSELIGQFGVGFYSAFL
Sbjct:    145  LHVTDTGVGMTREELVKNLGTIAKSGTSEFLNKMTEAQEDGQSTSELIGQFGVGFYSAFL 204
Conflict    188
TRAI       145  ++++++
Mature chain 145 *****

Query:     121  VADKVIVTSKHNDTQHIWESDSNEFSVIADPRGNTLGRGTTITLVLKEEASDYLELDTI 180
             VADKVIVTSKHNDTQHIWESDSNEFSVIADPRGNTLGRGTTITLVLKEEASDYLELDTI
Sbjct:    205  VADKVIVTSKHNDTQHIWESDSNEFSVIADPRGNTLGRGTTITLVLKEEASDYLELDTI 264
glycosylation 217
TRAI       205  ++++++
Mature chain 205 *****

Query:     181  KNLVKKYSQFINFPPIYVWSSKTETVEEPMEEEEAAKEEKEESDDEAAVEEEEEKKPKTK 240
             KNLVKKYSQFINFPPIYVWSSKTETVEEPMEEEEAAKEEKEESDDEAAVEEEEEKKPKTK
```

Sbjct: 265 KNLVKKYSQFINFPIYVWSSKTETVEEPMEEEEAAKEEKEESDDEAAVEEEEEKKPKTK 324
TRAI 265 ++++++
Mature chain 265 *****

Query: 241 KVEKTVDWELMNDIKPIWQRPSKEVEEDEYKAFYKSFSKESDDPMAYIHFTAEGEVTFK 300
KVEKTVDWELMNDIKPIWQRPSKEVEEDEYKAFYKSFSKESDDPMAYIHFTAEGEVTFK
Sbjct: 325 KVEKTVDWELMNDIKPIWQRPSKEVEEDEYKAFYKSFSKESDDPMAYIHFTAEGEVTFK 384
TRAI 325 ++++++
Mature chain 325 *****

Query: 301 SILFVPTSAPRGLFDEYGSKKSDYIKLYVRRVFITDDFHDMPKYLNFVKGVVDSDDLPL 360
SILFVPTSAPRGLFDEYGSKKSDYIKLYVRRVFITDDFHDMPKYLNFVKGVVDSDDLPL
Sbjct: 385 SILFVPTSAPRGLFDEYGSKKSDYIKLYVRRVFITDDFHDMPKYLNFVKGVVDSDDLPL 444
Conflict 419 *
TRAI 385 ++++++
Mature chain 385 *****

Query: 361 NVSRETQQHKLLKVIKRLVRKTLDMIKKIADDDKYNTFWKEFGTNIKLGVIEDHSNRT 420
NVSRETQQHKLLKVIKRLVRKTLDMIKKIADDDKYNTFWKEFGTNIKLGVIEDHSNRT
Sbjct: 445 NVSRETQQHKLLKVIKRLVRKTLDMIKKIADDDKYNTFWKEFGTNIKLGVIEDHSNRT 504
glycosylation 502 *
glycosylation 481 *
glycosylation 445 *
TRAI 445 ++++++
Mature chain 445 *****

Query: 421 RLAKLLRFQSSHHPTDITSLDQYVERMKEKQDKIYFMAGSSRKEAESSPFVERLLKKGYE 480
RLAKLLRFQSSHHPTDITSLDQYVERMKEKQDKIYFMAGSSRKEAESSPFVERLLKKGYE
Sbjct: 505 RLAKLLRFQSSHHPTDITSLDQYVERMKEKQDKIYFMAGSSRKEAESSPFVERLLKKGYE 564
TRAI 505 ++++++
Mature chain 505 *****

Query: 481 VIYLTEPVDEYCIQALPEFDGKRFQNVAKEGVKFDESEKTKESREAVEKEFEPLLNMWMD 540
VIYLTEPVDEYCIQALPEFDGKRFQNVAKEGVKFDESEKTKESREAVEKEFEPLLNMWMD
Sbjct: 565 VIYLTEPVDEYCIQALPEFDGKRFQNVAKEGVKFDESEKTKESREAVEKEFEPLLNMWMD 624
TRAI 565 ++++++
Mature chain 565 *****

Query: 541 KALKDKIEKAVVSQRLTESPCALVASQYGWSGNMERIMKAQAYQTGKDISTNYYASQKKT 600
KALKDKIEKAVVSQRLTESPCALVASQYGWSGNMERIMKAQAYQTGKDISTNYYASQKKT
Sbjct: 625 KALKDKIEKAVVSQRLTESPCALVASQYGWSGNMERIMKAQAYQTGKDISTNYYASQKKT 684
TRAI 625 ++++++
Mature chain 625 *****

Query: 601 FEINPRHPLIRDMLRRIKEDEDDKTVLDLAVVLFETATLRSGYLLPDTKAYGDRIERMLR 660
FEINPRHPLIRDMLRRIKEDEDDKTVLDLAVVLFETATLRSGYLLPDTKAYGDRIERMLR
Sbjct: 685 FEINPRHPLIRDMLRRIKEDEDDKTVLDLAVVLFETATLRSGYLLPDTKAYGDRIERMLR 744
TRAI 685 ++++++
Mature chain 685 *****

Query: 661 LSLNIDPDAKVEEPEEPEETAEDTTEDTEQDEDEEMDVGTDEEETAKESTAEDKDEL 719
LSLNIDPDAKVEEPEEPEETAEDTTEDTEQDEDEEMDVGTDEEETAKESTAEDKDEL
Sbjct: 745 LSLNIDPDAKVEEPEEPEETAEDTTEDTEQDEDEEMDVGTDEEETAKESTAEDKDEL 803
Conflict 803 *
other 800 ****
TRAI 745 ++++++
Mature chain 745 *****

CPU time: 0.17 user secs. 0.04 sys. secs 0.21 total secs.

Lambda K H
0.311 0.131 0.359

Gapped
Lambda K H

0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 14,675

Number of Sequences: 0

Number of extensions: 833

Number of successful extensions: 43

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3

length of query: 719

length of database: 330,426,180

effective HSP length: 131

effective length of query: 588

effective length of database: 270,223,427

effective search space: 158891375076

effective search space used: 158891375076

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.8 bits)

S2: 77 (34.3 bits)

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.